

SEQUENCE LISTING

<110> Lynglev, Gitte Budolfson
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Stringer, Mary Ann
Lange, Lene

<120> Method of Preparing a Heat-Treated Product

<130> 10347.204-US

<160> 15

<170> PatentIn version 3.3

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Ser Pro Leu Leu Tyr Pro Arg Ala Thr Asp Ser Asn Val Thr Tyr Val
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ttc acc aac ccc aat ggc ctg aac ttt act cag atg aac acc acc ctg 201
Phe Thr Asn Pro Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu
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cca aac gtc act atc ttc gcg aca ggc ggc aca atc gcg ggc tcc agc 249
Pro Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Ser
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Ala Asp Asn Thr Ala Thr Thr Gly Tyr Lys Ala Gly Ala Val Gly Ile
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cag aca ctg atc gac gcg gtc ccg gaa atg cta aac gtt gcc aac gtc 345
Gln Thr Leu Ile Asp Ala Val Pro Glu Met Leu Asn Val Ala Asn Val
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gct ggc gtg caa gta acc aat gtc ggc agc cca gac atc acc tcc gac 393
Ala Gly Val Gln Val Thr Asn Val Gly Ser Pro Asp Ile Thr Ser Asp

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att ctc ctg cgt ctc tcc aaa cag atc aac gag gtg gtc tgc aac gac Ile Leu Leu Arg Leu Ser Lys Gln Ile Asn Glu Val Val Cys Asn Asp	120	125	130	441
ccc acc atg gcc ggt gca gtg gtc acc cac ggc acc gac acg ctc gaa Pro Thr Met Ala Gly Ala Val Val Thr His Gly Thr Asp Thr Leu Glu	135	140	145	489
gaa tcc gcc ttc ttc ctc gac gcc acg gtc aac tgt cgc aag ccc gtg Glu Ser Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Arg Lys Pro Val	150	155	160	537
gtc atc gtc ggc gcc atg cgc cct tca acc gcc atc tcg gct gac ggc Val Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly	165	170	175	585
ccc ctc aac ctc ctg caa tcc gtc acc gtc gcc gcg agc ccc aag gcc Pro Leu Asn Leu Leu Gln Ser Val Thr Val Ala Ala Ser Pro Lys Ala	180	185	190	633
cga gac cgc ggc gcc ctg att gtc atg aac gac cgc atc gta tcc gcc Arg Asp Arg Gly Ala Leu Ile Val Met Asn Asp Arg Ile Val Ser Ala	200	205	210	681
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atc gaa atg ggt aac ctg ggc gag gtc gtc tcc aac aaa ccc tac ttc Ile Glu Met Gly Asn Leu Gly Glu Val Val Ser Asn Lys Pro Tyr Phe	230	235	240	777
ttc tac ccc cca gtc aag cca aca ggc aag acg gaa gta gat atc cgg Phe Tyr Pro Pro Val Lys Pro Thr Gly Lys Thr Glu Val Asp Ile Arg	245	250	255	825
aac atc acc tcc atc ccc aga gtc gac atc ctc tac tca tac gaa gac Asn Ile Thr Ser Ile Pro Arg Val Asp Ile Leu Tyr Ser Tyr Glu Asp	260	265	270	873
atg cac aat gac acc ctt tac tcc gcc atc gac aac ggc gca aag ggc Met His Asn Asp Thr Leu Tyr Ser Ala Ile Asp Asn Gly Ala Lys Gly	280	285	290	921
atc gtt atc gcc ggc tcc ggc tcc ggc tcc gtc tcc acc ccc ttc agc Ile Val Ile Ala Gly Ser Gly Ser Gly Ser Val Ser Thr Pro Phe Ser	295	300	305	969
gcc gcc atg gaa gac atc aca acc aaa cac aac atc ccc atc gta gcc Ala Ala Met Glu Asp Ile Thr Thr Lys His Asn Ile Pro Ile Val Ala	310	315	320	1017
agc acg cgc acc gga aac ggg gag gtg ccg tcc tcc gcc gag tcg agc Ser Thr Arg Thr Gly Asn Gly Glu Val Pro Ser Ser Ala Glu Ser Ser	325	330	335	1065

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 Gly Leu Leu Leu Ala Gln Gly Lys Ser Ile Glu Glu Met Arg Ala Val
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 <213> Aspergillus oryzae

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 35 40 45

Thr Thr Leu Pro Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala
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Gly Ser Ser Ala Asp Asn Thr Ala Thr Thr Gly Tyr Lys Ala Gly Ala
 65 70 75 80

Val Gly Ile Gln Thr Leu Ile Asp Ala Val Pro Glu Met Leu Asn Val
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Ala Asn Val Ala Gly Val Gln Val Thr Asn Val Gly Ser Pro Asp Ile
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Thr Ser Asp Ile Leu Leu Arg Leu Ser Lys Gln Ile Asn Glu Val Val
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Cys Asn Asp Pro Thr Met Ala Gly Ala Val Val Thr His Gly Thr Asp
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Thr Leu Glu Glu Ser Ala Phe Phe Leu Asp Ala Thr Val Asn Cys Arg
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Lys Pro Val Val Ile Val Gly Ala Met Arg Pro Ser Thr Ala Ile Ser
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Ala Asp Gly Pro Leu Asn Leu Leu Gln Ser Val Thr Val Ala Ala Ser
 180 185 190

Pro Lys Ala Arg Asp Arg Gly Ala Leu Ile Val Met Asn Asp Arg Ile
 195 200 205

Val Ser Ala Phe Tyr Ala Ser Lys Thr Asn Ala Asn Thr Val Asp Thr
 210 215 220

Phe Lys Ala Ile Glu Met Gly Asn Leu Gly Glu Val Val Ser Asn Lys
 225 230 235 240

Pro Tyr Phe Phe Tyr Pro Pro Val Lys Pro Thr Gly Lys Thr Glu Val
 245 250 255

Asp Ile Arg Asn Ile Thr Ser Ile Pro Arg Val Asp Ile Leu Tyr Ser
 260 265 270

Tyr Glu Asp Met His Asn Asp Thr Leu Tyr Ser Ala Ile Asp Asn Gly
 275 280 285

Ala Lys Gly Ile Val Ile Ala Gly Ser Gly Ser Gly Ser Val Ser Thr
 290 295 300

Pro Phe Ser Ala Ala Met Glu Asp Ile Thr Thr Lys His Asn Ile Pro
 305 310 315 320

Ile Val Ala Ser Thr Arg Thr Gly Asn Gly Glu Val Pro Ser Ser Ala
 325 330 335

Glu Ser Ser Gln Ile Ala Ser Gly Tyr Leu Asn Pro Ala Lys Ser Arg
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 Met Gly Leu Arg Val Lys Ala Leu
 1 5
 gca gtg gca gct ctg gct acc ctc agc cag gcc tcg ccg gtc cta tac 160
 Ala Val Ala Ala Leu Ala Thr Leu Ser Gln Ala Ser Pro Val Leu Tyr
 10 15 20
 act cgc gag gac act acc tcc aac aca acc tac gcc ttt acc aac agc 208
 Thr Arg Glu Asp Thr Thr Ser Asn Thr Thr Tyr Ala Phe Thr Asn Ser
 25 30 35 40
 aac ggg ctg aac ttc acc cag atg aac acc aca ctt cct aat gta acc 256
 Asn Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro Asn Val Thr
 45 50 55
 atc ttc gca aca g gtatgaccgt cccttcactt tcccatctct ttccaacccc 309
 Ile Phe Ala Thr
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 cttcagcaaa cagcaaacta aacaatagca acaacag gc ggc aca atc gcc ggc 363
 Gly Gly Thr Ile Ala Gly
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 tcg gcc gcc tct aac act gca aca aca ggc tac cag gcg ggc gcc ctc 411
 Ser Ala Ala Ser Asn Thr Ala Thr Thr Gly Tyr Gln Ala Gly Ala Leu
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 gga atc cag acc ctc atc gac gcc gtc ccc gaa atg ctc tcc gtc gcc 459
 Gly Ile Gln Thr Leu Ile Asp Ala Val Pro Glu Met Leu Ser Val Ala
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 aac atc gcc ggc gtg cag atc tcc aac gtc ggt agc cca gac gtc acc 507

Asn	Ile	Ala	Gly	Val	Gln	Ile	Ser	Asn	Val	Gly	Ser	Pro	Asp	Val	Thr		
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tcc	acc	atc	ctg	cta	gag	atg	gcg	cac	cgt	ctc	aac	aaa	gtt	gtc	tgc	555	
Ser	Thr	Ile	Leu	Leu	Glu	Met	Ala	His	Arg	Leu	Asn	Lys	Val	Val	Cys		
115					120				125						130		
gag	gac	cca	tcc	atg	gct	ggc	gca	gtc	gtc	acc	cac	ggc	act	gac	acc	603	
Glu	Asp	Pro	Ser	Met	Ala	Gly	Ala	Val	Val	Thr	His	Gly	Thr	Asp	Thr		
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ctt	gag	gaa	acg	gcc	ttc	ttc	ctc	gac	gca	aca	gtc	aac	tgc	ggg	aag	651	
Leu	Glu	Glu	Thr	Ala	Phe	Phe	Leu	Asp	Ala	Thr	Val	Asn	Cys	Gly	Lys		
			150					155					160				
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Pro	Ile	Val	Ile	Val	Gly	Ala	Met	Arg	Pro	Ala	Thr	Phe	Ile	Ser	Ala		
		165					170					175					
gat	ggg	ccc	tat	aat	ctc	ctg	cag	gcc	gtt	act	gtg	gcg	agc	acg	aaa	747	
Asp	Gly	Pro	Tyr	Asn	Leu	Leu	Gln	Ala	Val	Thr	Val	Ala	Ser	Thr	Lys		
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gag	gca	agg	aac	agg	ggc	gcg	atg	gtc	gtc	atg	aac	gac	cgc	atc	gcc	795	
Glu	Ala	Arg	Asn	Arg	Gly	Ala	Met	Val	Val	Met	Asn	Asp	Arg	Ile	Ala		
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Ser	Ala	Tyr	Tyr	Val	Ser	Lys	Thr	Asn	Ala	Asn	Thr	Met	Asp	Thr	Phe		
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Lys	Ala	Val	Glu	Met	Gly	Tyr	Leu	Gly	Ala	Ile	Ile	Ser	Asn	Thr	Pro		
			230					235					240				
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Phe	Phe	Tyr	Tyr	Pro	Ala	Val	Gln	Pro	Ser	Gly	Lys	Thr	Thr	Val	Asp		
		245					250					255					
gtg	tcc	aac	gtc	acc	tcc	atc	ccg	cgc	gtc	gac	atc	ctc	tac	tcc	ttc	987	
Val	Ser	Asn	Val	Thr	Ser	Ile	Pro	Arg	Val	Asp	Ile	Leu	Tyr	Ser	Phe		
	260					265					270						
cag	gac	atg	aca	aac	gac	acg	ctc	tac	tca	agc	att	gag	aac	ggc	gcg	1035	
Gln	Asp	Met	Thr	Asn	Asp	Thr	Leu	Tyr	Ser	Ser	Ile	Glu	Asn	Gly	Ala		
275					280					285					290		
aag	ggc	gtt	gtt	atc	gca	gga	tct	ggt	gct	ggg	agt	gtc	gat	acc	gcc	1083	
Lys	Gly	Val	Val	Ile	Ala	Gly	Ser	Gly	Ala	Gly	Ser	Val	Asp	Thr	Ala		
				295					300					305			
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Phe	Ser	Thr	Ala	Ile	Asp	Asp	Ile	Ile	Ser	Asn	Gln	Gly	Val	Pro	Ile		
			310					315					320				
gtg	cag	agt	act	agg	aca	gga	aac	gga	gag	gtg	ccg	tat	tcg	gct	gag	1179	
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340	345	350	
ttg gga ttg ctg ttg gcc cag gga ggg aag ggc act gaa gaa att agg			1275
Leu Gly Leu Leu Leu Ala Gln Gly Gly Lys Gly Thr Glu Glu Ile Arg			
355	360	365	370
gcg gtg ttt ggg aag gtt gct gtt tgattcccgga ctgcccagggt cttatgatgt			1329
Ala Val Phe Gly Lys Val Ala Val			
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Asn Thr Thr Leu Pro Asn Val Thr Ile Phe Ala Thr Gly Gly Thr Ile
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Ala Gly Ser Ala Ala Ser Asn Thr Ala Thr Thr Gly Tyr Gln Ala Gly
65 70 75 80

Ala Leu Gly Ile Gln Thr Leu Ile Asp Ala Val Pro Glu Met Leu Ser
85 90 95

Val Ala Asn Ile Ala Gly Val Gln Ile Ser Asn Val Gly Ser Pro Asp
100 105 110

Val Thr Ser Thr Ile Leu Leu Glu Met Ala His Arg Leu Asn Lys Val
115 120 125

Val Cys Glu Asp Pro Ser Met Ala Gly Ala Val Val Thr His Gly Thr
 130 135 140

Asp Thr Leu Glu Glu Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys
 145 150 155 160

Gly Lys Pro Ile Val Ile Val Gly Ala Met Arg Pro Ala Thr Phe Ile
 165 170 175

Ser Ala Asp Gly Pro Tyr Asn Leu Leu Gln Ala Val Thr Val Ala Ser
 180 185 190

Thr Lys Glu Ala Arg Asn Arg Gly Ala Met Val Val Met Asn Asp Arg
 195 200 205

Ile Ala Ser Ala Tyr Tyr Val Ser Lys Thr Asn Ala Asn Thr Met Asp
 210 215 220

Thr Phe Lys Ala Val Glu Met Gly Tyr Leu Gly Ala Ile Ile Ser Asn
 225 230 235 240

Thr Pro Phe Phe Tyr Tyr Pro Ala Val Gln Pro Ser Gly Lys Thr Thr
 245 250 255

Val Asp Val Ser Asn Val Thr Ser Ile Pro Arg Val Asp Ile Leu Tyr
 260 265 270

Ser Phe Gln Asp Met Thr Asn Asp Thr Leu Tyr Ser Ser Ile Glu Asn
 275 280 285

Gly Ala Lys Gly Val Val Ile Ala Gly Ser Gly Ala Gly Ser Val Asp
 290 295 300

Thr Ala Phe Ser Thr Ala Ile Asp Asp Ile Ile Ser Asn Gln Gly Val
 305 310 315 320

Pro Ile Val Gln Ser Thr Arg Thr Gly Asn Gly Glu Val Pro Tyr Ser
 325 330 335

Ala Glu Gly Gly Ile Ser Ser Gly Phe Leu Asn Pro Ala Lys Ser Arg
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Ile Leu Leu Gly Leu Leu Leu Ala Gln Gly Gly Lys Gly Thr Glu Glu
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Ile Arg Ala Val Phe Gly Lys Val Ala Val
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 <222> (93)..(978)

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 Met Thr Lys Leu Ser Phe Lys
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 atc atc aca ctc gcg gct atg ata gcc gtt ggg aat gcc tct ccg ttt 161
 Ile Ile Thr Leu Ala Ala Met Ile Ala Val Gly Asn Ala Ser Pro Phe
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 gtc tac ccc cga gca acc agc cca aac agt aca tat gtc ttc acc aac 209
 Val Tyr Pro Arg Ala Thr Ser Pro Asn Ser Thr Tyr Val Phe Thr Asn
 25 30 35
 tcg cat ggc ttg aac ttc acc cag atg aac acg acg ctc cct aat gtc 257
 Ser His Gly Leu Asn Phe Thr Gln Met Asn Thr Thr Leu Pro Asn Val
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 acc atc ctc gca acc ggc ggt acc att gcc ggc tcc agc aac gac aac 305
 Thr Ile Leu Ala Thr Gly Gly Thr Ile Ala Gly Ser Ser Asn Asp Asn
 60 65 70
 acc gcc aca aca ggc tac acg gcc ggc gcg atc ggc atc cag cag ctc 353
 Thr Ala Thr Thr Gly Tyr Thr Ala Gly Ala Ile Gly Ile Gln Gln Leu
 75 80 85
 atg gat gcc gtc cct gag atg cta gac gtt gct aac gtg gcc ggc atc 401
 Met Asp Ala Val Pro Glu Met Leu Asp Val Ala Asn Val Ala Gly Ile
 90 95 100
 cag gtc gcc aat gtc ggc agc ccc gac gtg acg tct tcc ctt ctg ctc 449
 Gln Val Ala Asn Val Gly Ser Pro Asp Val Thr Ser Ser Leu Leu Leu
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cac atg gcc agg acc atc aac gag gtc gtc tgc gac gac ccc acc atg His Met Ala Arg Thr Ile Asn Glu Val Val Cys Asp Asp Pro Thr Met 120 125 130 135	497
agc ggc gcc gtc atc acg cac ggc acc gac acg ctc gag gag acg gcc Ser Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala 140 145 150	545
ttc ttc ctc gac gct aca gtc aac tgc ggc aag ccc atc gtc gtc gtc Phe Phe Leu Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val Val Val 155 160 165	593
ggc gcc atg cgg ccc gca acc gcc atc tcc gcc gac ggc ccg ttc aac Gly Ala Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Phe Asn 170 175 180	641
ctc ctc cag gcc gtg acc gtc gcc gcg cac ccc act gcg cgc aac cgt Leu Leu Gln Ala Val Thr Val Ala Ala His Pro Thr Ala Arg Asn Arg 185 190 195	689
ggt gcg ctg gtc gtc atg aac gac cgc att gtg tcc gcg tac tac gtc Gly Ala Leu Val Val Met Asn Asp Arg Ile Val Ser Ala Tyr Tyr Val 200 205 210 215	737
tcc aag aca aac gcc aac acc atg gac acc ttc aag gcc gtc gag atg Ser Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Val Glu Met 220 225 230	785
ggc aac ctc ggc gcc atc atc tcc aac aag ccg tac ttc ttt tac ccg Gly Asn Leu Gly Ala Ile Ile Ser Asn Lys Pro Tyr Phe Phe Tyr Pro 235 240 245	833
ccc gtc atg ccc acc ggt aag acc act ttc gac gtg cgc aac gtc gcc Pro Val Met Pro Thr Gly Lys Thr Thr Phe Asp Val Arg Asn Val Ala 250 255 260	881
tcc atc ccc aga gtc gac atc ctc tac tcg tac cag gat atg caa aac Ser Ile Pro Arg Val Asp Ile Leu Tyr Ser Tyr Gln Asp Met Gln Asn 265 270 275	929
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 Ser Gly Phe Leu Asn Pro Gln Lys Ala Arg Ile Leu Leu Gly Leu Leu
 340 345 350
 ctt gct gag gat aag gga ttc aag gag atc aaa gag gcg ttc gcg aag 1279
 Leu Ala Glu Asp Lys Gly Phe Lys Glu Ile Lys Glu Ala Phe Ala Lys
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 Asn Gly Val Ala

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 <213> *Aspergillus fumigatus*

<400> 6

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 35 40 45

Asn Thr Thr Leu Pro Asn Val Thr Ile Leu Ala Thr Gly Gly Thr Ile
 50 55 60

Ala Gly Ser Ser Asn Asp Asn Thr Ala Thr Thr Gly Tyr Thr Ala Gly
 65 70 75 80

Ala Ile Gly Ile Gln Gln Leu Met Asp Ala Val Pro Glu Met Leu Asp
 85 90 95

Val Ala Asn Val Ala Gly Ile Gln Val Ala Asn Val Gly Ser Pro Asp
 100 105 110

Val Thr Ser Ser Leu Leu Leu His Met Ala Arg Thr Ile Asn Glu Val
 115 120 125

Val Cys Asp Asp Pro Thr Met Ser Gly Ala Val Ile Thr His Gly Thr
 130 135 140

Asp Thr Leu Glu Glu Thr Ala Phe Phe Leu Asp Ala Thr Val Asn Cys
 145 150 155 160

Gly Lys Pro Ile Val Val Val Gly Ala Met Arg Pro Ala Thr Ala Ile
 165 170 175

Ser Ala Asp Gly Pro Phe Asn Leu Leu Gln Ala Val Thr Val Ala Ala
 180 185 190

His Pro Thr Ala Arg Asn Arg Gly Ala Leu Val Val Met Asn Asp Arg
 195 200 205

Ile Val Ser Ala Tyr Tyr Val Ser Lys Thr Asn Ala Asn Thr Met Asp
 210 215 220

Thr Phe Lys Ala Val Glu Met Gly Asn Leu Gly Ala Ile Ile Ser Asn
 225 230 235 240

Lys Pro Tyr Phe Phe Tyr Pro Pro Val Met Pro Thr Gly Lys Thr Thr
 245 250 255

Phe Asp Val Arg Asn Val Ala Ser Ile Pro Arg Val Asp Ile Leu Tyr
 260 265 270

Ser Tyr Gln Asp Met Gln Asn Asp Thr Leu Tyr Asp Ala Val Asp Asn
 275 280 285

Gly Ala Lys Gly Ile Val Val Arg Ser Val Ser Ser Gly Tyr Tyr Asp
 290 295 300

Ala Ile Asp Asp Ile Ala Ser Thr His Ser Leu Pro Val Val Leu Ser
 305 310 315 320

Thr Arg Thr Gly Asn Gly Glu Val Ala Ile Thr Asp Ser Glu Thr Thr
 325 330 335

Ile Glu Ser Gly Phe Leu Asn Pro Gln Lys Ala Arg Ile Leu Leu Gly
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Leu Leu Leu Ala Glu Asp Lys Gly Phe Lys Glu Ile Lys Glu Ala Phe
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Ala Lys Asn Gly Val Ala

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 <213> Fusarium graminearum

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 Met Ser Pro Ser
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 Phe His Ser Leu Leu Ala Ile Ala Thr Leu Ala Gly Ser Ala Ala Leu
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 Ala Ser Pro Ile Pro Glu Pro Glu Thr Pro Gln Leu Ile Pro Arg Ala
 25 30 35
 gtt ggt gac ttt gag tgc ttc aac gct agt ctt ccc aac atc acc atc 260
 Val Gly Asp Phe Glu Cys Phe Asn Ala Ser Leu Pro Asn Ile Thr Ile
 40 45 50
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 Thr Thr Gly Tyr Gln Ala Gly Ala Leu Gly Ile Gln Ala Leu Ile Asp
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 Ala Val Pro Gln Leu Cys Asn Val Ser Asn Val Arg Gly Val Gln Ile
 85 90 95 100
 gcc aac gtt gat agc ggc gat gta aac tct act atc ctg acc act ttg 452
 Ala Asn Val Asp Ser Gly Asp Val Asn Ser Thr Ile Leu Thr Thr Leu
 105 110 115
 gcg cat cgc atc cag act gat ctt gac aac cct cac atc caa ggt gtt 500
 Ala His Arg Ile Gln Thr Asp Leu Asp Asn Pro His Ile Gln Gly Val
 120 125 130
 gtc gtc acc cat ggc aca gac act ctc gag gag tct tca ttt ttc ctc 548
 Val Val Thr His Gly Thr Asp Thr Leu Glu Glu Ser Ser Phe Phe Leu
 135 140 145
 gat ctc act gtc caa agt gaa aag cct gtt gtt atg gtt gga tcc atg 596

Asp	Leu	Thr	Val	Gln	Ser	Glu	Lys	Pro	Val	Val	Met	Val	Gly	Ser	Met	
150						155					160					
cgt	cct	gcc	act	gcc	atc	agc	gct	gat	ggc	ccc	atc	aac	ctc	ctg	tct	644
Arg	Pro	Ala	Thr	Ala	Ile	Ser	Ala	Asp	Gly	Pro	Ile	Asn	Leu	Leu	Ser	
165					170					175					180	
gct	gtt	cga	ttg	gca	ggc	agc	aag	agt	gcc	aag	ggc	cgc	ggc	aca	atg	692
Ala	Val	Arg	Leu	Ala	Gly	Ser	Lys	Ser	Ala	Lys	Gly	Arg	Gly	Thr	Met	
				185					190					195		
att	gta	ctc	aac	gac	aag	atc	gct	tct	gca	cgc	tac	acc	gtt	aaa	tcc	740
Ile	Val	Leu	Asn	Asp	Lys	Ile	Ala	Ser	Ala	Arg	Tyr	Thr	Val	Lys	Ser	
			200					205					210			
cac	gcc	aat	gct	gtc	cag	act	ttc	att	gcc	gaa	gat	caa	ggc	tat	ctt	788
His	Ala	Asn	Ala	Val	Gln	Thr	Phe	Ile	Ala	Glu	Asp	Gln	Gly	Tyr	Leu	
		215					220					225				
ggc	gcc	ttt	gaa	aac	att	cag	ccc	gtc	ttc	tgg	tac	cct	gct	agt	cga	836
Gly	Ala	Phe	Glu	Asn	Ile	Gln	Pro	Val	Phe	Trp	Tyr	Pro	Ala	Ser	Arg	
	230					235					240					
cca	cta	ggc	cac	cac	tat	ttc	aac	att	agt	gct	agc	tca	cct	aag	aag	884
Pro	Leu	Gly	His	His	Tyr	Phe	Asn	Ile	Ser	Ala	Ser	Ser	Pro	Lys	Lys	
245					250					255					260	
gct	ctt	cct	cag	gtt	gac	gtt	ttg	tac	ggc	cac	caa	gaa	gcg	gac	ccc	932
Ala	Leu	Pro	Gln	Val	Asp	Val	Leu	Tyr	Gly	His	Gln	Glu	Ala	Asp	Pro	
				265					270					275		
gag	ctt	ttc	caa	gct	gct	gtc	gat	agc	ggc	gcc	cag	ggc	att	gtt	ctc	980
Glu	Leu	Phe	Gln	Ala	Ala	Val	Asp	Ser	Gly	Ala	Gln	Gly	Ile	Val	Leu	
			280					285					290			
gct	ggc	ctt	ggc	gct	gga	ggc	tgg	cct	gac	gaa	gct	gct	gat	gag	atc	1028
Ala	Gly	Leu	Gly	Ala	Gly	Gly	Trp	Pro	Asp	Glu	Ala	Ala	Asp	Glu	Ile	
		295					300					305				
aag	aag	gtc	ttg	aac	gag	act	aac	att	cct	gtt	gtt	gtc	agc	cgt	cgt	1076
Lys	Lys	Val	Leu	Asn	Glu	Thr	Asn	Ile	Pro	Val	Val	Val	Ser	Arg	Arg	
	310					315					320					
act	gct	tgg	ggc	tac	gtt	gga	gag	agg	cct	ttc	ggc	atc	ggc	gct	ggg	1124
Thr	Ala	Trp	Gly	Tyr	Val	Gly	Glu	Arg	Pro	Phe	Gly	Ile	Gly	Ala	Gly	
325					330					335					340	
tac	ttg	aac	cct	tcc	aag	gcc	aga	atc	caa	ctg	caa	ctt	gcg	ctt	gag	1172
Tyr	Leu	Asn	Pro	Ser	Lys	Ala	Arg	Ile	Gln	Leu	Gln	Leu	Ala	Leu	Glu	
				345					350					355		
aag	aag	ctt	tct	gtg	gag	gag	atc	caa	gac	ata	ttc	gag	tat	gtt		1217
Lys	Lys	Leu	Ser	Val	Glu	Glu	Ile	Gln	Asp	Ile	Phe	Glu	Tyr	Val		
		360						365				370				
tgattggaag	aggattttga	aatgaatcaa	tgatatatga	tta												1260

<210> 8
 <211> 371
 <212> PRT
 <213> Fusarium graminearum

<400> 8

Met Ser Pro Ser Phe His Ser Leu Leu Ala Ile Ala Thr Leu Ala Gly
 1 5 10 15

Ser Ala Ala Leu Ala Ser Pro Ile Pro Glu Pro Glu Thr Pro Gln Leu
 20 25 30

Ile Pro Arg Ala Val Gly Asp Phe Glu Cys Phe Asn Ala Ser Leu Pro
 35 40 45

Asn Ile Thr Ile Phe Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Gly
 50 55 60

Ser Ala Asp Gln Thr Thr Gly Tyr Gln Ala Gly Ala Leu Gly Ile Gln
 65 70 75 80

Ala Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ser Asn Val Arg
 85 90 95

Gly Val Gln Ile Ala Asn Val Asp Ser Gly Asp Val Asn Ser Thr Ile
 100 105 110

Leu Thr Thr Leu Ala His Arg Ile Gln Thr Asp Leu Asp Asn Pro His
 115 120 125

Ile Gln Gly Val Val Val Thr His Gly Thr Asp Thr Leu Glu Glu Ser
 130 135 140

Ser Phe Phe Leu Asp Leu Thr Val Gln Ser Glu Lys Pro Val Val Met
 145 150 155 160

Val Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Ile
 165 170 175

Asn Leu Leu Ser Ala Val Arg Leu Ala Gly Ser Lys Ser Ala Lys Gly
 180 185 190

Arg Gly Thr Met Ile Val Leu Asn Asp Lys Ile Ala Ser Ala Arg Tyr

195		200		205
Thr Val Lys Ser His Ala Asn Ala Val Gln Thr Phe Ile Ala Glu Asp				
210		215		220
Gln Gly Tyr Leu Gly Ala Phe Glu Asn Ile Gln Pro Val Phe Trp Tyr				
225		230		235
Pro Ala Ser Arg Pro Leu Gly His His Tyr Phe Asn Ile Ser Ala Ser				
	245		250	255
Ser Pro Lys Lys Ala Leu Pro Gln Val Asp Val Leu Tyr Gly His Gln				
	260		265	270
Glu Ala Asp Pro Glu Leu Phe Gln Ala Ala Val Asp Ser Gly Ala Gln				
	275		280	285
Gly Ile Val Leu Ala Gly Leu Gly Ala Gly Gly Trp Pro Asp Glu Ala				
290		295		300
Ala Asp Glu Ile Lys Lys Val Leu Asn Glu Thr Asn Ile Pro Val Val				
305		310		315
Val Ser Arg Arg Thr Ala Trp Gly Tyr Val Gly Glu Arg Pro Phe Gly				
	325		330	335
Ile Gly Ala Gly Tyr Leu Asn Pro Ser Lys Ala Arg Ile Gln Leu Gln				
	340		345	350
Leu Ala Leu Glu Lys Lys Leu Ser Val Glu Glu Ile Gln Asp Ile Phe				
	355		360	365
Glu Tyr Val				
370				

<210> 9
 <211> 1470
 <212> DNA
 <213> Fusarium graminearum

<220>
 <221> CDS
 <222> (77)..(1429)

<400> 9
aggacaagcg tccatgaagc ataactacgc tacattgcct ttagctacag ttgatctata 60
gatatcagtc tacatc atg atg ccc agc gtc aga aga ttt cac ggc cag act 112
Met Met Pro Ser Val Arg Arg Phe His Gly Gln Thr
1 5 10
atg gtc gcc gcc gct cct tct att tgc tca ggg cct gca gca tcg tcc 160
Met Val Ala Ala Ala Pro Ser Ile Cys Ser Gly Pro Ala Ala Ser Ser
15 20 25
acc atc aag atg gct tca tcg tca gct tcg tgg acg act tat ctg tgg 208
Thr Ile Lys Met Ala Ser Ser Ser Ala Ser Trp Thr Thr Tyr Leu Trp
30 35 40
cgg ctt atc cta gct gtg ctg gct cct tca acg gcc ctg ctg cct ttt 256
Arg Leu Ile Leu Ala Val Leu Ala Pro Ser Thr Ala Leu Leu Pro Phe
45 50 55 60
ggg gcg tgg gtt gtt tcg gtc tgg gga tct cct gtc ctc gac cta cac 304
Gly Ala Trp Val Val Ser Val Trp Gly Ser Pro Val Leu Asp Leu His
65 70 75
gtc caa cct cac ttc tcg gtt caa caa aaa gcg cca ata cag acg ggc 352
Val Gln Pro His Phe Ser Val Gln Gln Lys Ala Pro Ile Gln Thr Gly
80 85 90
atc cct ttc gaa att tcg acc acc tca gga ttc aac tgc ttc aat ccc 400
Ile Pro Phe Glu Ile Ser Thr Thr Ser Gly Phe Asn Cys Phe Asn Pro
95 100 105
aat ctt ccc aac gtc act att tat gcc acc gga ggt act att gct ggc 448
Asn Leu Pro Asn Val Thr Ile Tyr Ala Thr Gly Gly Thr Ile Ala Gly
110 115 120
tcc gca agc tcg gct gat cag acc acg gga tac cgg tca gct gcg tta 496
Ser Ala Ser Ser Ala Asp Gln Thr Thr Gly Tyr Arg Ser Ala Ala Leu
125 130 135 140
gga gtt gat tct ctc att gat gca gta ccc caa ttg tgc aat gta gcc 544
Gly Val Asp Ser Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ala
145 150 155
aat gtg aga ggt gtc cag ttt gcc aac acg gac agc ata gac atg agc 592
Asn Val Arg Gly Val Gln Phe Ala Asn Thr Asp Ser Ile Asp Met Ser
160 165 170
tcg gcc atg ttg agg act ttg gcg aag cag atc cag aat gat ctg gac 640
Ser Ala Met Leu Arg Thr Leu Ala Lys Gln Ile Gln Asn Asp Leu Asp
175 180 185
agt ccg ttt act caa ggc gca gtt gtg acg cac gga act gat act ctg 688
Ser Pro Phe Thr Gln Gly Ala Val Val Thr His Gly Thr Asp Thr Leu
190 195 200
gat gaa tct gcc ttc ttt ctg gat ctt act atc cag agc gac aag ccc 736
Asp Glu Ser Ala Phe Phe Leu Asp Leu Thr Ile Gln Ser Asp Lys Pro

205	210	215	220	
gtg gtc gtg aca ggc tca atg cgc ccg gca act gct atc agc gca gat Val Val Val Thr Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp 225 230 235				784
gga cca atg aat ctt ttg tca tcg gtg aca ttg gca gca gca gcg agt Gly Pro Met Asn Leu Leu Ser Ser Val Thr Leu Ala Ala Ala Ala Ser 240 245 250				832
gct cga ggc aga gga gtg atg att gcc atg aat gat cgc att gga tct Ala Arg Gly Arg Gly Val Met Ile Ala Met Asn Asp Arg Ile Gly Ser 255 260 265				880
gct cgt ttt acg acc aaa gtc aac gcc aac cat ttg gac gcc ttc caa Ala Arg Phe Thr Thr Lys Val Asn Ala Asn His Leu Asp Ala Phe Gln 270 275 280				928
gcc cct gac agt ggc atg ctg gga aca ttc gtc aac gtt cag cca gtg Ala Pro Asp Ser Gly Met Leu Gly Thr Phe Val Asn Val Gln Pro Val 285 290 295 300				976
ttt ttc tat ccg cca tca cga cct ctt ggc cac cgt cat ttt gat ctg Phe Phe Tyr Pro Pro Ser Arg Pro Leu Gly His Arg His Phe Asp Leu 305 310 315				1024
cgg ccc atc acc aac aac ggc cgc cgg ttc gga cgc tct aca gcc ccc Arg Pro Ile Thr Asn Asn Gly Arg Arg Phe Gly Arg Ser Thr Ala Pro 320 325 330				1072
gga gca gga tca tca gca cta ccc cag gtg gac gtg ctc tac gct tac Gly Ala Gly Ser Ser Ala Leu Pro Gln Val Asp Val Leu Tyr Ala Tyr 335 340 345				1120
cag gag ctc agc gtg ggc atg ttc cag gcg gcc atc gac ctt gga gcg Gln Glu Leu Ser Val Gly Met Phe Gln Ala Ala Ile Asp Leu Gly Ala 350 355 360				1168
cag ggc atc gtt cta gcg gga atg ggc gct gga ttc tgg acg tcc aaa Gln Gly Ile Val Leu Ala Gly Met Gly Ala Gly Phe Trp Thr Ser Lys 365 370 375 380				1216
ggc acc gag gag att cgg cgt atc gtc cac gag acc gat att ccc gtg Gly Thr Glu Glu Ile Arg Arg Ile Val His Glu Thr Asp Ile Pro Val 385 390 395				1264
ata gtg agc cga aga ccg gaa ggc ggc ttc gtc gga cca tgt gag gca Ile Val Ser Arg Arg Pro Glu Gly Gly Phe Val Gly Pro Cys Glu Ala 400 405 410				1312
gga atc ggc gcg ggc ttt ttg aat ccg caa aag gcg agg atc cag ctc Gly Ile Gly Ala Gly Phe Leu Asn Pro Gln Lys Ala Arg Ile Gln Leu 415 420 425				1360
caa ctg gcc ctg gag acc aag atg gac aat gat gcc atc aaa gcc ctg Gln Leu Ala Leu Glu Thr Lys Met Asp Asn Asp Ala Ile Lys Ala Leu 430 435 440				1408

ttt gag cat tcg gga gtg cac taaagggaca aaaaagatcg aggttacagc 1459
Phe Glu His Ser Gly Val His
445 450

agcaacacca c 1470

<210> 10
<211> 451
<212> PRT
<213> *Fusarium graminearum*

<400> 10

Met Met Pro Ser Val Arg Arg Phe His Gly Gln Thr Met Val Ala Ala
1 5 10 15

Ala Pro Ser Ile Cys Ser Gly Pro Ala Ala Ser Ser Thr Ile Lys Met
20 25 30

Ala Ser Ser Ser Ala Ser Trp Thr Thr Tyr Leu Trp Arg Leu Ile Leu
35 40 45

Ala Val Leu Ala Pro Ser Thr Ala Leu Leu Pro Phe Gly Ala Trp Val
50 55 60

Val Ser Val Trp Gly Ser Pro Val Leu Asp Leu His Val Gln Pro His
65 70 75 80

Phe Ser Val Gln Gln Lys Ala Pro Ile Gln Thr Gly Ile Pro Phe Glu
85 90 95

Ile Ser Thr Thr Ser Gly Phe Asn Cys Phe Asn Pro Asn Leu Pro Asn
100 105 110

Val Thr Ile Tyr Ala Thr Gly Gly Thr Ile Ala Gly Ser Ala Ser Ser
115 120 125

Ala Asp Gln Thr Thr Gly Tyr Arg Ser Ala Ala Leu Gly Val Asp Ser
130 135 140

Leu Ile Asp Ala Val Pro Gln Leu Cys Asn Val Ala Asn Val Arg Gly
145 150 155 160

Val Gln Phe Ala Asn Thr Asp Ser Ile Asp Met Ser Ser Ala Met Leu
165 170 175

Arg Thr Leu Ala Lys Gln Ile Gln Asn Asp Leu Asp Ser Pro Phe Thr
 180 185 190

Gln Gly Ala Val Val Thr His Gly Thr Asp Thr Leu Asp Glu Ser Ala
 195 200 205

Phe Phe Leu Asp Leu Thr Ile Gln Ser Asp Lys Pro Val Val Val Thr
 210 215 220

Gly Ser Met Arg Pro Ala Thr Ala Ile Ser Ala Asp Gly Pro Met Asn
 225 230 235 240

Leu Leu Ser Ser Val Thr Leu Ala Ala Ala Ala Ser Ala Arg Gly Arg
 245 250 255

Gly Val Met Ile Ala Met Asn Asp Arg Ile Gly Ser Ala Arg Phe Thr
 260 265 270

Thr Lys Val Asn Ala Asn His Leu Asp Ala Phe Gln Ala Pro Asp Ser
 275 280 285

Gly Met Leu Gly Thr Phe Val Asn Val Gln Pro Val Phe Phe Tyr Pro
 290 295 300

Pro Ser Arg Pro Leu Gly His Arg His Phe Asp Leu Arg Pro Ile Thr
 305 310 315 320

Asn Asn Gly Arg Arg Phe Gly Arg Ser Thr Ala Pro Gly Ala Gly Ser
 325 330 335

Ser Ala Leu Pro Gln Val Asp Val Leu Tyr Ala Tyr Gln Glu Leu Ser
 340 345 350

Val Gly Met Phe Gln Ala Ala Ile Asp Leu Gly Ala Gln Gly Ile Val
 355 360 365

Leu Ala Gly Met Gly Ala Gly Phe Trp Thr Ser Lys Gly Thr Glu Glu
 370 375 380

Ile Arg Arg Ile Val His Glu Thr Asp Ile Pro Val Ile Val Ser Arg
 385 390 395 400

Arg Pro Glu Gly Gly Phe Val Gly Pro Cys Glu Ala Gly Ile Gly Ala
405 410 415

Gly Phe Leu Asn Pro Gln Lys Ala Arg Ile Gln Leu Gln Leu Ala Leu
420 425 430

Glu Thr Lys Met Asp Asn Asp Ala Ile Lys Ala Leu Phe Glu His Ser
435 440 445

Gly Val His
450

<210> 11
<211> 1236
<212> DNA
<213> Penicillium citrinum

<220>
<221> CDS
<222> (16)..(1152)

<400> 11
acatattgaa acaat atg aga ctt cta ttt aat act ctg gct gtc tca gca 51
Met Arg Leu Leu Phe Asn Thr Leu Ala Val Ser Ala
1 5 10

cta gct gct acg agt tat gcc tct ccc atc att cat tcc cgg gcc tcc 99
Leu Ala Ala Thr Ser Tyr Ala Ser Pro Ile Ile His Ser Arg Ala Ser
15 20 25

aac acg tcc tat acc aac tct aat ggg ctg aaa ttt aac cat ttc gac 147
Asn Thr Ser Tyr Thr Asn Ser Asn Gly Leu Lys Phe Asn His Phe Asp
30 35 40

gct tct ctt cca aat gtg act ttg ctg gca act ggt gga act att gcc 195
Ala Ser Leu Pro Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala
45 50 55 60

ggt aca agc gat gac aag act gct acg gca gga tat gaa tcc ggg gct 243
Gly Thr Ser Asp Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala
65 70 75

tta ggg ata aat aag att ctt tcc ggc atc cca gaa gtt tat gac att 291
Leu Gly Ile Asn Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile
80 85 90

gcc aac gtc aat gcg gta cag ttt gac aat gtc aac agc ggc gat gtc 339
Ala Asn Val Asn Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val
95 100 105

tct yca tct ctc tta ctg aac atg aca cat acc ctt caa aag acc gtt 387

Ser	Xaa	Ser	Leu	Leu	Leu	Asn	Met	Thr	His	Thr	Leu	Gln	Lys	Thr	Val		
110						115					120						
tgt	gat	gac	cct	acg	ata	tct	ggc	gcc	gtc	atc	acc	cat	ggc	acc	gat	435	
Cys	Asp	Asp	Pro	Thr	Ile	Ser	Gly	Ala	Val	Ile	Thr	His	Gly	Thr	Asp		
125					130					135					140		
acc	ctg	gaa	gaa	tct	gcc	ttc	ttc	atc	gat	gca	aca	gtc	aac	tgc	ggc	483	
Thr	Leu	Glu	Glu	Ser	Ala	Phe	Phe	Ile	Asp	Ala	Thr	Val	Asn	Cys	Gly		
				145					150					155			
aag	ccg	att	gtg	ttc	gtt	ggc	tca	atg	cga	cct	tcc	acc	gca	atc	tct	531	
Lys	Pro	Ile	Val	Phe	Val	Gly	Ser	Met	Arg	Pro	Ser	Thr	Ala	Ile	Ser		
			160					165					170				
gcc	gat	ggc	cct	atg	aat	ttg	ctc	cag	gga	gtg	act	gtg	gcc	gct	gac	579	
Ala	Asp	Gly	Pro	Met	Asn	Leu	Leu	Gln	Gly	Val	Thr	Val	Ala	Ala	Asp		
		175					180					185					
aaa	cag	gct	aag	aac	cgc	gga	gca	cta	gtc	gtg	ctg	aat	gac	cgc	att	627	
Lys	Gln	Ala	Lys	Asn	Arg	Gly	Ala	Leu	Val	Val	Leu	Asn	Asp	Arg	Ile		
	190					195					200						
gtc	tct	gct	ttc	ttc	gct	aca	aag	aca	aat	gcg	aat	aca	atg	gac	act	675	
Val	Ser	Ala	Phe	Phe	Ala	Thr	Lys	Thr	Asn	Ala	Asn	Thr	Met	Asp	Thr		
205					210					215					220		
ttc	aag	gct	tat	gaa	caa	ggc	agt	ctt	ggc	atg	att	gtt	tca	aac	aag	723	
Phe	Lys	Ala	Tyr	Glu	Gln	Gly	Ser	Leu	Gly	Met	Ile	Val	Ser	Asn	Lys		
				225					230					235			
ccc	tac	ttc	tat	tat	ccg	gca	gtc	gag	cca	aac	gcg	aag	cac	gtt	gtt	771	
Pro	Tyr	Phe	Tyr	Tyr	Pro	Ala	Val	Glu	Pro	Asn	Ala	Lys	His	Val	Val		
			240					245					250				
cat	ctt	gac	gac	gtg	gat	gcg	atc	ccc	cgt	gtg	gat	att	ctc	tac	gct	819	
His	Leu	Asp	Asp	Val	Asp	Ala	Ile	Pro	Arg	Val	Asp	Ile	Leu	Tyr	Ala		
		255					260					265					
tac	gag	gac	atg	cat	agc	gac	tcc	ctt	cac	agt	gct	atc	aaa	aat	gga	867	
Tyr	Glu	Asp	Met	His	Ser	Asp	Ser	Leu	His	Ser	Ala	Ile	Lys	Asn	Gly		
	270					275					280						
gcc	aag	ggc	atc	gtg	gtc	gcc	ggc	gag	ggc	gca	ggt	ggt	atc	tcc	acg	915	
Ala	Lys	Gly	Ile	Val	Val	Ala	Gly	Glu	Gly	Ala	Gly	Gly	Ile	Ser	Thr		
285					290					295					300		
gac	ttt	agt	gat	acc	atc	gat	gag	att	gca	tcg	aag	cat	cag	att	ccc	963	
Asp	Phe	Ser	Asp	Thr	Ile	Asp	Glu	Ile	Ala	Ser	Lys	His	Gln	Ile	Pro		
				305					310					315			
att	atc	ctg	agc	cac	aga	acc	gtg	aac	gga	gaa	gtt	cct	act	gct	gat	1011	
Ile	Ile	Leu	Ser	His	Arg	Thr	Val	Asn	Gly	Glu	Val	Pro	Thr	Ala	Asp		
			320					325					330				
att	acg	ggt	gat	agc	gcg	aag	act	cgc	att	gca	agt	ggc	atg	tat	aac	1059	
Ile	Thr	Gly	Asp	Ser	Ala	Lys	Thr	Arg	Ile	Ala	Ser	Gly	Met	Tyr	Asn		

335	340	345	
ccc cag cag gcg cgc gtc ttg ctt gga cta ttg ctc gca gaa ggc aag			1107
Pro Gln Gln Ala Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys			
350	355	360	
aag ttt gag gat att cga act atc ttc gga aaa gct act gtt gcc			1152
Lys Phe Glu Asp Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala			
365	370	375	
tagacccacg tcatatatta tgcccatact tgggaacact tgaaactgat agactaaatt			1212
aattatattg tcgtttgttg ccgg			1236

<210> 12
 <211> 379
 <212> PRT
 <213> Penicillium citrinum

 <220>
 <221> misc_feature
 <222> (110)..(110)
 <223> The 'Xaa' at location 110 stands for Pro, or Ser.

 <400> 12

Met Arg Leu Leu Phe Asn Thr Leu Ala Val Ser Ala Leu Ala Ala Thr			
1	5	10	15
Ser Tyr Ala Ser Pro Ile Ile His Ser Arg Ala Ser Asn Thr Ser Tyr			
20	25	30	
Thr Asn Ser Asn Gly Leu Lys Phe Asn His Phe Asp Ala Ser Leu Pro			
35	40	45	
Asn Val Thr Leu Leu Ala Thr Gly Gly Thr Ile Ala Gly Thr Ser Asp			
50	55	60	
Asp Lys Thr Ala Thr Ala Gly Tyr Glu Ser Gly Ala Leu Gly Ile Asn			
65	70	75	80
Lys Ile Leu Ser Gly Ile Pro Glu Val Tyr Asp Ile Ala Asn Val Asn			
85	90	95	
Ala Val Gln Phe Asp Asn Val Asn Ser Gly Asp Val Ser Xaa Ser Leu			
100	105	110	
Leu Leu Asn Met Thr His Thr Leu Gln Lys Thr Val Cys Asp Asp Pro			
115	120	125	

Thr Ile Ser Gly Ala Val Ile Thr His Gly Thr Asp Thr Leu Glu Glu
 130 135 140

Ser Ala Phe Phe Ile Asp Ala Thr Val Asn Cys Gly Lys Pro Ile Val
 145 150 155 160

Phe Val Gly Ser Met Arg Pro Ser Thr Ala Ile Ser Ala Asp Gly Pro
 165 170 175

Met Asn Leu Leu Gln Gly Val Thr Val Ala Ala Asp Lys Gln Ala Lys
 180 185 190

Asn Arg Gly Ala Leu Val Val Leu Asn Asp Arg Ile Val Ser Ala Phe
 195 200 205

Phe Ala Thr Lys Thr Asn Ala Asn Thr Met Asp Thr Phe Lys Ala Tyr
 210 215 220

Glu Gln Gly Ser Leu Gly Met Ile Val Ser Asn Lys Pro Tyr Phe Tyr
 225 230 235 240

Tyr Pro Ala Val Glu Pro Asn Ala Lys His Val Val His Leu Asp Asp
 245 250 255

Val Asp Ala Ile Pro Arg Val Asp Ile Leu Tyr Ala Tyr Glu Asp Met
 260 265 270

His Ser Asp Ser Leu His Ser Ala Ile Lys Asn Gly Ala Lys Gly Ile
 275 280 285

Val Val Ala Gly Glu Gly Ala Gly Gly Ile Ser Thr Asp Phe Ser Asp
 290 295 300

Thr Ile Asp Glu Ile Ala Ser Lys His Gln Ile Pro Ile Ile Leu Ser
 305 310 315 320

His Arg Thr Val Asn Gly Glu Val Pro Thr Ala Asp Ile Thr Gly Asp
 325 330 335

Ser Ala Lys Thr Arg Ile Ala Ser Gly Met Tyr Asn Pro Gln Gln Ala
 340 345 350

Arg Val Leu Leu Gly Leu Leu Leu Ala Glu Gly Lys Lys Phe Glu Asp
 355 360 365

Ile Arg Thr Ile Phe Gly Lys Ala Thr Val Ala
 370 375

<210> 13
 <211> 362
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 13

Met Arg Ser Leu Asn Thr Leu Leu Leu Ser Leu Phe Val Ala Met Ser
 1 5 10 15

Ser Gly Ala Pro Leu Leu Lys Ile Arg Glu Glu Lys Asn Ser Ser Leu
 20 25 30

Pro Ser Ile Lys Ile Phe Gly Thr Gly Gly Thr Ile Ala Ser Lys Gly
 35 40 45

Ser Thr Ser Ala Thr Thr Ala Gly Tyr Ser Val Gly Leu Thr Val Asn
 50 55 60

Asp Leu Ile Glu Ala Val Pro Ser Leu Ala Glu Lys Ala Asn Leu Asp
 65 70 75 80

Tyr Leu Gln Val Ser Asn Val Gly Ser Asn Ser Leu Asn Tyr Thr His
 85 90 95

Leu Ile Pro Leu Tyr His Gly Ile Ser Glu Ala Leu Ala Ser Asp Asp
 100 105 110

Tyr Ala Gly Ala Val Val Thr His Gly Thr Asp Thr Met Glu Glu Thr
 115 120 125

Ala Phe Phe Leu Asp Leu Thr Ile Asn Ser Glu Lys Pro Val Cys Ile
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Ala Gly Ala Met Arg Pro Ala Thr Ala Thr Ser Ala Asp Gly Pro Met
 145 150 155 160

Asn Leu Tyr Gln Ala Val Ser Ile Ala Ala Ser Glu Lys Ser Leu Gly

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Arg	Gly	Thr	Met	Ile	Thr	Leu	Asn	Asp	Arg	Ile	Ala	Ser	Gly	Phe	Trp
			180					185					190		
Thr	Thr	Lys	Met	Asn	Ala	Asn	Ser	Leu	Asp	Thr	Phe	Arg	Ala	Asp	Glu
		195					200					205			
Gln	Gly	Tyr	Leu	Gly	Tyr	Phe	Ser	Asn	Asp	Asp	Val	Glu	Phe	Tyr	Tyr
	210					215					220				
Pro	Pro	Val	Lys	Pro	Asn	Gly	Trp	Gln	Phe	Phe	Asp	Ile	Ser	Asn	Leu
225					230					235					240
Thr	Asp	Pro	Ser	Glu	Ile	Pro	Glu	Val	Ile	Ile	Leu	Tyr	Ser	Tyr	Gln
				245					250					255	
Gly	Leu	Asn	Pro	Glu	Leu	Ile	Val	Lys	Ala	Val	Lys	Asp	Leu	Gly	Ala
			260					265					270		
Lys	Gly	Ile	Val	Leu	Ala	Gly	Ser	Gly	Ala	Gly	Ser	Trp	Thr	Ala	Thr
		275					280					285			
Gly	Ser	Ile	Val	Asn	Glu	Gln	Leu	Tyr	Glu	Glu	Tyr	Gly	Ile	Pro	Ile
	290					295					300				
Val	His	Ser	Arg	Arg	Thr	Ala	Asp	Gly	Thr	Val	Pro	Pro	Asp	Asp	Ala
305					310					315					320
Pro	Glu	Tyr	Ala	Ile	Gly	Ser	Gly	Tyr	Leu	Asn	Pro	Gln	Lys	Ser	Arg
				325					330					335	
Ile	Leu	Leu	Gln	Leu	Cys	Leu	Tyr	Ser	Gly	Tyr	Gly	Met	Asp	Gln	Ile
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Arg	Ser	Val	Phe	Ser	Gly	Val	Tyr	Gly	Gly						
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